



SEQUENCE LISTING

<110> LEDBETTER, JEFFREY
HAYDEN-LEDBETTER, MARTHA

<120> DNA VACCINES ENCODING ANTIGEN LINKED TO A DOMAIN THAT BINDS CD40

<130> 034474.0003 UTL1

<140> 09/687,864

<141> 2000-10-13

<150> US 60/159,690

<151> 1999-10-14

<160> 29

<170> PatentIn Ver. 3.2

<210> 1

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1

agcttgccgc catgctgtat acctctcagc tgtaggact acttctgttt tggatctcgg 60
cttcga 66

<210> 2

<211> 67

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2

gatctcgaag cccgagatcc aaaacagaag tagtcctaac agctgagagg tatacagcat 60
ggcggca 67

<210> 3

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3

gttgctggat ccagaaaaca gctttgaaat gcaa

34

<210> 4
 <211> 44
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 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

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 <211> 35
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 5
 gttgtcggat ccaagaaggt tggacaagat agaag 35

 <210> 6
 <211> 27
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Primer

 <400> 6
 ggatattgat gagatctagt gctacag 27

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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Primer

 <400> 7
 gaacacagct cctattggat ccggtctttt ttctctttgc ac 42

 <210> 8
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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Primer

<400> 8
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 tttttctctt tgcactgttc ttctctttgc 90

<210> 9
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9
 gttattccat ggatccggac taatcttaca atgtgcttg 39

<210> 10
 <211> 32
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Primer

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 gtacagctaa atagatctgt agtaattaat tg 32

<210> 11
 <211> 93
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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 aatgttacaa tgtgcttggt gtcttatatc tcc 93

<210> 12
 <211> 2252
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 HIV-human fusion construct

<220>
 <221> CDS
 <222> (13)..(2238)

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<220>
<221> sig_peptide
<222> (13)..(72)

<220>
<221> mat_peptide
<222> (73)..(2238)

<220>
<221> misc_feature
<222> (73)..(1587)
<223> HIV gp120 allele + (Gly4Ser)3 linker

<220>
<221> misc_feature
<222> (1594)..(2238)
<223> CD154 extracellular domain from amino acids 48-261+Glu
      binds to CD40

<400> 12
aagcttgccg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20              -15              -10

tgg atc tcg gct tcg aga tct atg ctc ctt ggg ata ttg atg atc tgt    99
Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
      -5              -1    1              5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg    147
Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
      10              15              20              25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc    195
Trp Arg Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
      30              35              40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc    243
Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
      45              50              55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat    291
Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
      60              65              70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata    339
Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
      75              80              85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca    387
Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
      90              95              100              105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act    435
Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
      110              115              120

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act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata	483
Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile	
125 130 135	
aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag	531
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys	
140 145 150	
aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat	579
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn	
155 160 165	
act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att	627
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile	
170 175 180 185	
aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat	675
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr	
190 195 200	
tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc	723
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe	
205 210 215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat	771
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His	
220 225 230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta	819
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Asn Gly Ser Leu	
235 240 245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct	867
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala	
250 255 260 265	
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca	915
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr	
270 275 280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga	963
Arg Pro Asn Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg	
285 290 295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat	1011
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His	
300 305 310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt	1059
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val	
315 320 325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa	1107
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln	
330 335 340 345	

tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga	1155
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly	
350 355 360	
ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg	1203
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp	
365 370 375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca	1251
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr	
380 385 390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga	1299
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly	
395 400 405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca	1347
Lys Ala Met Tyr Ala Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser	
410 415 420 425	
aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag	1395
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu	
430 435 440	
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat	1443
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn	
445 450 455	
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata	1491
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile	
460 465 470	
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa	1539
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys	
475 480 485	
aga ggg gga ggc ggt tca gga ggt gga ggt tct gga ggt ggc gga tcg	1587
Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser	
490 495 500 505	
gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt cat gaa	1635
Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu	
510 515 520	
gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga gaa aga	1683
Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg	
525 530 535	
tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt gaa ggc	1731
Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly	
540 545 550	
ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa gaa aac	1779
Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn	
555 560 565	

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agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg gca cat 1827
Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His
570                      575                      580                      585

gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag tgg gct 1875
Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala
                    590                      595                      600

gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg gaa aat 1923
Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn
                    605                      610                      615

ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc tat gcc 1971
Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala
                    620                      625                      630

caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct cca ttt 2019
Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe
                    635                      640                      645

ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga atc tta 2067
Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu
650                      655                      660                      665

ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg caa caa 2115
Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln
                    670                      675                      680

tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct tcg gtg 2163
Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val
                    685                      690                      695

ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act ggc ttc 2211
Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe
                    700                      705                      710

acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta gata 2252
Thr Ser Phe Gly Leu Leu Lys Leu Glu
715                      720

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<210> 13

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> CDS

<222> (13)..(2196)

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<222> (13)..(72)

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<221> mat_peptide
<222> (73)..(2196)

<220>
<221> misc_feature
<222> (73)..(1545)
<223> HIV gp120 allele + ProAspPro linker

<220>
<221> misc_feature
<222> (1552)..(2196)
<223> CD154 extracellular domain long form (amino acids 48-261)+Glu
      binds to CD40

<400> 13
aagcttgccg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20              -15              -10

tgg atc tcg gct tcg aga tcc atg ctc ctt ggg ata ttg atg atc tgt    99
Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
      -5              -1    1              5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg    147
Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
      10              15              20              25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc    195
Trp Arg Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
      30              35              40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc    243
Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
      45              50              55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat    291
Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
      60              65              70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata    339
Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
      75              80              85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca    387
Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
      90              95              100              105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act    435
Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
      110              115              120

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act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata	483
Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile	
125 130 135	
aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag	531
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys	
140 145 150	
aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat	579
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn	
155 160 165	
act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att	627
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile	
170 175 180 185	
aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat	675
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr	
190 195 200	
tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc	723
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe	
205 210 215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat	771
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His	
220 225 230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta	819
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Asn Gly Ser Leu	
235 240 245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct	867
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala	
250 255 260 265	
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca	915
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr	
270 275 280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga	963
Arg Pro Asn Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg	
285 290 295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat	1011
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His	
300 305 310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt	1059
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val	
315 320 325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa	1107
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln	
330 335 340 345	

tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga	1155
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly	
350 355 360	
ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg	1203
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp	
365 370 375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca	1251
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr	
380 385 390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga	1299
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly	
395 400 405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca	1347
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser	
410 415 420 425	
aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag	1395
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu	
430 435 440	
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat	1443
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn	
445 450 455	
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata	1491
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile	
460 465 470	
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa	1539
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys	
475 480 485	
aga ccg gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt	1587
Arg Pro Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu	
490 495 500 505	
cat gaa gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga	1635
His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly	
510 515 520	
gaa aga tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt	1683
Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe	
525 530 535	
gaa ggc ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa	1731
Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys	
540 545 550	
gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg	1779
Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala	
555 560 565	

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gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag 1827
Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln
570                    575                    580                    585

tggt gct gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg 1875
Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu
590                    595                    600

gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc 1923
Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile
605                    610                    615

tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct 1971
Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala
620                    625                    630

cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga 2019
Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg
635                    640                    645

atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg 2067
Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly
650                    655                    660                    665

caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct 2115
Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala
670                    675                    680

tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act 2163
Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr
685                    690                    695

ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga 2208
Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
700                    705

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<210> 14

<211> 2070

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> CDS

<222> (13)..(2058)

<220>

<221> sig_peptide

<222> (13)..(72)

<220>
 <221> mat_peptide
 <222> (73)..(2058)

<220>
 <221> misc_feature
 <222> (73)..(1587)
 <223> HIV gp120 allele + (Gly4Ser)3 linker

<220>
 <221> misc_feature
 <222> (1594)..(2058)
 <223> CD154 extracellular domain from amino acids 108-261+Glu
 binds to CD40

<400> 14
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 Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Phe
 -20 -15 -10

tgg atc tcg gct tcg aga tct atg ctc ctt ggg ata ttg atg atc tgt 99
 Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
 -5 -1 1 5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
 Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
 10 15 20 25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
 Trp Arg Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
 30 35 40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
 Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
 45 50 55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
 Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
 60 65 70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
 Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
 75 80 85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
 Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
 90 95 100 105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
 Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
 110 115 120

act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata 483
 Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile
 125 130 135

aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag	531
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys	
140 145 150	
aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat	579
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn	
155 160 165	
act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att	627
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile	
170 175 180 185	
aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat	675
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr	
190 195 200	
tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc	723
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe	
205 210 215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat	771
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His	
220 225 230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta	819
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu	
235 240 245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct	867
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala	
250 255 260 265	
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca	915
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr	
270 275 280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga	963
Arg Pro Asn Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg	
285 290 295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat	1011
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His	
300 305 310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt	1059
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val	
315 320 325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa	1107
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln	
330 335 340 345	
tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga	1155
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly	
350 355 360	

ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg	1203
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp	
365 370 375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca	1251
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr	
380 385 390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga	1299
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly	
395 400 405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca	1347
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser	
410 415 420 425	
aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag	1395
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu	
430 435 440	
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat	1443
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn	
445 450 455	
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata	1491
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile	
460 465 470	
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa	1539
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys	
475 480 485	
aga ggg gga ggc ggt tca gga ggt gga ggt tct gga ggt ggc gga tcg	1587
Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser	
490 495 500 505	
gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa	1635
Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln	
510 515 520	
att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg	1683
Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val	
525 530 535	
tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac ttg gta	1731
Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val	
540 545 550	
acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat	1779
Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr	
555 560 565	
tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt	1827
Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser	
570 575 580 585	

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caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc 1875
Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe
                    590                    595                    600

gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct 1923
Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro
                    605                    610                    615

tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca 1971
Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro
                    620                    625                    630

ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat 2019
Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His
                    635                    640                    645

ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga 2070
Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
650                    655                    660

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<210> 15

<211> 2028

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> CDS

<222> (13)..(2016)

<220>

<221> sig_peptide

<222> (13)..(72)

<220>

<221> mat_peptide

<222> (73)..(2016)

<220>

<221> misc_feature

<222> (73)..(1551)

<223> HIV gp120 allele + ProAspPro linker

<220>

<221> misc_feature

<222> (1552)..(2016)

<223> CD154 extracellular domain from amino acids 108-261+Glu
binds to CD40

<400> 15
aagcttgccg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
-20 -15 -10

tgg atc tcg gct tcg aga tcc atg ctc ctt ggg ata ttg atg atc tgt 99
Trp Ile Ser Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys
-5 -1 1 5

agt gct aca gaa aaa ttg tgg gtc aca gtc tat tat ggg gta cct gtg 147
Ser Ala Thr Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
10 15 20 25

tgg aga gaa gca acc acc act cta ttt tgt gca tca gat gct aaa gcc 195
Trp Arg Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
30 35 40

tat gat aca gag gta cat aat gtt tgg gcc aca cat gcc tgt gta ccc 243
Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
45 50 55

aca gac ccc aac cca caa gaa gta gta ttg gga aat gtg aca gaa aat 291
Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn
60 65 70

ttt aac atg tgg aaa aat aac atg gta gat cag atg cat gag gat ata 339
Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
75 80 85

atc agt tta tgg gat gaa agc cta aag cca tgt gta aaa tta acc cca 387
Ile Ser Leu Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
90 95 100 105

ctc tgt gtt act tta aat tgc act aat ttg aat atc act aag aat act 435
Leu Cys Val Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr
110 115 120

act aat ccc act agt agc agc tgg gga atg atg gag aaa gga gaa ata 483
Thr Asn Pro Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile
125 130 135

aaa aat tgc tct ttc tat atc acc aca agc ata aga aat aag gta aag 531
Lys Asn Cys Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys
140 145 150

aaa gaa tat gca ctt ttt aat aga ctt gat gta gta cca ata gaa aat 579
Lys Glu Tyr Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn
155 160 165

act aat aat act aag tat agg tta ata agt tgt aac acc tca gtc att 627
Thr Asn Asn Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile
170 175 180 185

aca cag gcc tgt cca aag gta tcc ttt cag cca att ccc ata cat tat 675
Thr Gln Ala Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr
190 195 200

tgt gtc ccg gct ggg ttt gcg atg cta aag tgt aac aat aag aca ttc	723
Cys Val Pro Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe	
205 210 215	
aat gga tca gga cca tgc aca aat gtc agc aca gta caa tgt aca cat	771
Asn Gly Ser Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His	
220 225 230	
gga att agg cca gtg gtg tca act caa ctg ctg tta aat ggc agt cta	819
Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu	
235 240 245	
gca gaa gaa gac ata gta att aga tct gaa aat ttc aca gac aat gct	867
Ala Glu Glu Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala	
250 255 260 265	
aaa acc ata ata gta cag cta aat gaa tct gta gta att aat tgt aca	915
Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr	
270 275 280	
aga ccc aac aac aat aca aga aga agg tta tct ata gga cca ggg aga	963
Arg Pro Asn Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg	
285 290 295	
gca ttt tat gca aga aga aac ata ata gga gat ata aga caa gca cat	1011
Ala Phe Tyr Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His	
300 305 310	
tgt aac att agt aga gca aaa tgg aat aac act tta caa cag ata gtt	1059
Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val	
315 320 325	
ata aaa tta aga gaa aaa ttt agg aat aaa aca ata gcc ttt aat caa	1107
Ile Lys Leu Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln	
330 335 340 345	
tcc tca gga ggg gac cca gaa att gta atg cac agt ttt aat tgt gga	1155
Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly	
350 355 360	
ggg gaa ttc ttc tac tgt aat aca gca caa ctg ttt aat agt act tgg	1203
Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp	
365 370 375	
aat gtt act gga ggg aca aat ggc act gaa gga aat gac ata atc aca	1251
Asn Val Thr Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr	
380 385 390	
ctc caa tgc aga ata aaa caa att ata aat atg tgg cag aaa gta gga	1299
Leu Gln Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly	
395 400 405	
aaa gca atg tat gcc cct ccc atc aca gga caa att aga tgt tca tca	1347
Lys Ala Met Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser	
410 415 420 425	

aat att aca ggg ctg cta cta aca aga gat gga ggt aat agt act gag	1395
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu	
430 435 440	
act gag act gag atc ttc aga cct gga gga gga gat atg agg gac aat	1443
Thr Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn	
445 450 455	
tgg aga agt gaa tta tat aaa tat aaa gta gta aga att gaa cca ata	1491
Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile	
460 465 470	
gga gta gca ccc acc agg gca aag aga aga aca gtg caa aga gaa aaa	1539
Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys	
475 480 485	
aga ccg gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat	1587
Arg Pro Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn	
490 495 500 505	
cct caa att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca	1635
Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr	
510 515 520	
tct gtg tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac	1683
Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn	
525 530 535	
ttg gta acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga	1731
Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly	
540 545 550	
ctc tat tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct	1779
Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala	
555 560 565	
tcg agt caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt	1827
Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly	
570 575 580 585	
aga ttc gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc	1875
Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala	
590 595 600	
aaa cct tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg	1923
Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu	
605 610 615	
caa cca ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg	1971
Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val	
620 625 630	
agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag	2016
Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu	
635 640 645	
tgataatcta ga	2028

<210> 16
 <211> 906
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 HIV-human fusion construct

<220>
 <221> CDS
 <222> (13)..(894)

<220>
 <221> sig_peptide
 <222> (13)..(72)

<220>
 <221> mat_peptide
 <222> (73)..(894)

<220>
 <221> misc_feature
 <222> (73)..(243)
 <223> HIV gp120 V3 loop + (Gly4Ser)3 linker

<220>
 <221> misc_feature
 <222> (250)..(894)
 <223> CD154 extracellular domain from amino acids 48-261+Glu
 binds to CD40

<400> 16
 aagcttgccg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
 Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
 -20 -15 -10

tgg atc tcg gct tcg aga tct gta gta att aat tgt aca aga ccc aac 99
 Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 -5 -1 1 5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat 147
 Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 10 15 20 25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att 195
 Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 30 35 40

agt ggt ggc ggt ggc tca gga ggc ggt gga tct ggc ggt gga ggt tcg 243
 Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 45 50 55

gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt cat gaa	291
Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu	
60 65 70	
gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga gaa aga	339
Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg	
75 80 85	
tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt gaa ggc	387
Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly	
90 95 100 105	
ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa gaa aac	435
Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn	
110 115 120	
agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg gca cat	483
Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His	
125 130 135	
gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag tgg gct	531
Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala	
140 145 150	
gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg gaa aat	579
Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn	
155 160 165	
ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc tat gcc	627
Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala	
170 175 180 185	
caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct cca ttt	675
Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe	
190 195 200	
ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga atc tta	723
Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu	
205 210 215	
ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg caa caa	771
Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln	
220 225 230	
tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct tcg gtg	819
Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val	
235 240 245	
ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act ggc ttc	867
Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe	
250 255 260 265	
acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga	906
Thr Ser Phe Gly Leu Lys Leu Glu	
270	

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<210> 17
<211> 864
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> CDS
<222> (13)..(852)

<220>
<221> sig_peptide
<222> (13)..(72)

<220>
<221> mat_peptide
<222> (73)..(852)

<220>
<221> misc_feature
<222> (73)..(207)
<223> HIV gp120 allele + (Gly4Ser)3 linker

<220>
<221> misc_feature
<222> (208)..(852)
<223> CD154 extracellular domain from amino acids 48-261+Glu
      binds to CD40

<400> 17
aagcttgccg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Phe
      -20                -15                -10

tgg atc tcg gct tcg aga tct gta gta att aat tgt aca aga ccc aac 99
Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
      -5                -1    1                5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat 147
Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
      10                15                20                25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att 195
Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
      30                35                40

agt ccg gat cca aga agg ttg gac aag ata gaa gat gaa agg aat ctt 243
Ser Pro Asp Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu
      45                50                55

cat gaa gat ttt gta ttc atg aaa acg ata cag aga tgc aac aca gga 291
His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly
      60                65                70

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gaa aga tcc tta tcc tta ctg aac tgt gag gag att aaa agc cag ttt	339
Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe	
75 80 85	
gaa ggc ttt gtg aag gat ata atg tta aac aaa gag gag acg aag aaa	387
Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys	
90 95 100 105	
gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa att gcg	435
Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala	
110 115 120	
gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg tta cag	483
Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln	
125 130 135	
tgg gct gaa aaa gga tac tac acc atg agc aac aac ttg gta acc ctg	531
Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu	
140 145 150	
gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat tat atc	579
Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile	
155 160 165	
tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt caa gct	627
Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala	
170 175 180 185	
cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc gag aga	675
Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg	
190 195 200	
atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct tgc ggg	723
Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly	
205 210 215	
caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca ggt gct	771
Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala	
220 225 230	
tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat ggc act	819
Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr	
235 240 245	
ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga	864
Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu	
250 255 260	

<210> 18

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> CDS

<222> (13)..(714)

<220>

<221> sig_peptide

<222> (13)..(72)

<220>

<221> mat_peptide

<222> (73)..(714)

<220>

<221> misc_feature

<222> (73)..(207)

<223> HIV gp120 V3 loop + ProAspPro linker

<220>

<221> misc_feature

<222> (208)..(714)

<223> CD154 extracellular domain from amino acids 108-261+Glu
binds to CD40

<400> 18

```

aagcttgccg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Phe
      -20                      -15                      -10

tgg atc tcg gct tcg aga tct gta gta att aat tgt aca aga ccc aac   99
Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
      -5                      -1    1                      5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat   147
Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
      10                      15                      20                      25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att   195
Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
      30                      35                      40

agt ggt ggc ggt ggc tca gga ggc ggt gga tct ggc ggt gga ggt tcg   243
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
      45                      50                      55

gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat cct caa   291
Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln
      60                      65                      70

att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca tct gtg   339
Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val
      75                      80                      85

```

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tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac ttg gta 387
Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val
90 95 100 105

acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga ctc tat 435
Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr
110 115 120

tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt 483
Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser
125 130 135

caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt aga ttc 531
Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe
140 145 150

gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc aaa cct 579
Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro
155 160 165

tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg caa cca 627
Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro
170 175 180 185

ggg gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg agc cat 675
Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His
190 195 200

ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag tgataatcta ga 726
Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
205 210

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<210> 19

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> CDS

<222> (13)..(672)

<220>

<221> sig_peptide

<222> (13)..(72)

<220>

<221> mat_peptide

<222> (73)..(672)


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<220>
<221> misc_feature
<222> (73)..(207)
<223> HIV gp120 V3 loop + ProAspPro linker

<220>
<221> misc_feature
<222> (208)..(672)
<223> CD154 extracellular domain from amino acids 108-261+Glu
      binds to CD40

<400> 19
aagcttgccg cc atg ctg tat acc tct cag ctg tta gga cta ctt ctg ttt 51
      Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe
      -20                      -15                      -10

tgg atc tcg gct tcg aga tct gta gta att aat tgt aca aga ccc aac 99
Trp Ile Ser Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn
      -5                      -1      1                      5

aac aat aca aga aga agg tta tct ata gga cca ggg aga gca ttt tat 147
Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
      10                      15                      20                      25

gca aga aga aac ata ata gga gat ata aga caa gca cat tgt aac att 195
Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
      30                      35                      40

agt ccg gat cca gaa aac agc ttt gaa atg caa aaa ggt gat cag aat 243
Ser Pro Asp Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn
      45                      50                      55

cct caa att gcg gca cat gtc ata agt gag gcc agc agt aaa aca aca 291
Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr
      60                      65                      70

tct gtg tta cag tgg gct gaa aaa gga tac tac acc atg agc aac aac 339
Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn
      75                      80                      85

ttg gta acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga caa gga 387
Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly
      90                      95                      100                      105

ctc tat tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg gaa gct 435
Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala
      110                      115                      120

tcg agt caa gct cca ttt ata gcc agc ctc tgc cta aag tcc ccc ggt 483
Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly
      125                      130                      135

aga ttc gag aga atc tta ctc aga gct gca aat acc cac agt tcc gcc 531
Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala
      140                      145                      150

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aaa cct tgc ggg caa caa tcc att cac ttg gga gga gta ttt gaa ttg   579
Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu
      155                      160                      165

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```

caa cca ggt gct tcg gtg ttt gtc aat gtg act gat cca agc caa gtg   627
Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val
      170                      175                      180                      185

```

```

agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc gag   672
Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
              190                      195                      200

```

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tgataatcta ga   684

```

<210> 20

<211> 742

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(526)

<223> HIV gp120 domain with (Gly4Ser)3 linker

<220>

<221> BINDING

<222> (529)..(742)

<223> CD154 extracellular domain long form amino acids 48(Arg) to
261(Leu) + Glu binds CD40

<400> 20

```

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20                      -15                      -10                      -5

```

```

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
      -1      1                      5                      10

```

```

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
      15                      20                      25

```

```

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
      30                      35                      40

```

```

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
      45                      50                      55                      60

```

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
 65 70 75
 Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
 80 85 90
 Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
 95 100 105
 Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr Thr Asn Pro
 110 115 120
 Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile Lys Asn Cys
 125 130 135 140
 Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys Lys Glu Tyr
 145 150 155
 Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn Thr Asn Asn
 160 165 170
 Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala
 175 180 185
 Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr Cys Val Pro
 190 195 200
 Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Ser
 205 210 215 220
 Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
 225 230 235
 Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu
 240 245 250
 Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile
 255 260 265
 Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 270 275 280
 Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 285 290 295 300
 Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 305 310 315
 Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val Ile Lys Leu
 320 325 330
 Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln Ser Ser Gly
 335 340 345
 Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 350 355 360

Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 365 370 375 380
 Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395
 Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 400 405 410
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 415 420 425
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 430 435 440
 Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 445 450 455 460
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 465 470 475
 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Gly Gly
 480 485 490
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Arg
 495 500 505
 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
 510 515 520
 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
 525 530 535 540
 Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
 545 550 555
 Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
 560 565 570
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 575 580 585
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 590 595 600
 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 605 610 615 620
 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 625 630 635
 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 640 645 650
 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 655 660 665

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
670 675 680

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
685 690 695 700

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
705 710 715

Gly Leu Leu Lys Leu Glu
720

<210> 21
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide

<220>
<221> DOMAIN
<222> (21)..(513)
<223> HIV gp120 domain with ProAspPro linker

<220>
<221> BINDING
<222> (514)..(728)
<223> CD154 extracellular domain long form amino acids 48(Arg) to
261(Leu) + Glu binds CD40

<400> 21
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20 -15 -10 -5

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
-1 1 5 10

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
15 20 25

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
30 35 40

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
45 50 55 60

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
65 70 75

Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
 80 85 90
 Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
 95 100 105
 Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr Thr Asn Pro
 110 115 120
 Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile Lys Asn Cys
 125 130 135 140
 Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys Lys Glu Tyr
 145 150 155
 Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn Thr Asn Asn
 160 165 170
 Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala
 175 180 185
 Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr Cys Val Pro
 190 195 200
 Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Ser
 205 210 215 220
 Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
 225 230 235
 Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu
 240 245 250
 Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile
 255 260 265
 Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 270 275 280
 Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 285 290 295 300
 Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 305 310 315
 Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val Ile Lys Leu
 320 325 330
 Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln Ser Ser Gly
 335 340 345
 Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 350 355 360
 Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 365 370 375 380

Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395
 Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 400 405 410
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 415 420 425
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 430 435 440
 Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 445 450 455 460
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 465 470 475
 Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Pro Asp
 480 485 490
 Pro Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
 495 500 505
 Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
 510 515 520
 Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
 525 530 535 540
 Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
 545 550 555
 Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
 560 565 570
 Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
 575 580 585
 Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
 590 595 600
 Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
 605 610 615 620
 Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
 625 630 635
 Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
 640 645 650
 Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
 655 660 665
 Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
 670 675 680

Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
685 690 695 700

Ser Phe Gly Leu Leu Lys Leu Glu
705

<210> 22

<211> 682

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(525)

<223> HIV gp120 domain with (Gly4Ser)3 linker

<220>

<221> BINDING

<222> (528)..(682)

<223> CD154 extracellular domain long form amino acids 108(Glu) to
261(Leu) + Glu binds CD40

<400> 22

Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20 -15 -10 -5

Ala Ser Arg Ser Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr
-1 1 5 10

Glu Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Arg Glu
15 20 25

Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr
30 35 40

Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
45 50 55 60

Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Asn Phe Asn Met
65 70 75

Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
80 85 90

Trp Asp Glu Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
 95 100 105
 Thr Leu Asn Cys Thr Asn Leu Asn Ile Thr Lys Asn Thr Thr Asn Pro
 110 115 120
 Thr Ser Ser Ser Trp Gly Met Met Glu Lys Gly Glu Ile Lys Asn Cys
 125 130 135 140
 Ser Phe Tyr Ile Thr Thr Ser Ile Arg Asn Lys Val Lys Lys Glu Tyr
 145 150 155
 Ala Leu Phe Asn Arg Leu Asp Val Val Pro Ile Glu Asn Thr Asn Asn
 160 165 170
 Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala
 175 180 185
 Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr Cys Val Pro
 190 195 200
 Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Ser
 205 210 215 220
 Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
 225 230 235
 Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu
 240 245 250
 Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile
 255 260 265
 Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 270 275 280
 Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 285 290 295 300
 Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 305 310 315
 Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val Ile Lys Leu
 320 325 330
 Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln Ser Ser Gly
 335 340 345
 Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 350 355 360
 Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 365 370 375 380
 Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395

```

Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
      400                      405                      410

Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
      415                      420                      425

Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
      430                      435                      440

Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
      445                      450                      455                      460

Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
      465                      470                      475

Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Gly Gly
      480                      485                      490

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Glu
      495                      500                      505

Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala
      510                      515                      520

His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
      525                      530                      535                      540

Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu
      545                      550                      555

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
      560                      565                      570

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
      575                      580                      585

Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
      590                      595                      600

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
      605                      610                      615                      620

Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
      625                      630                      635

Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
      640                      645                      650

Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
      655                      660

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<210> 23

<211> 668

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(513)

<223> HIV gp120 domain with ProAspPro linker

<220>

<221> BINDING

<222> (514)..(668)

<223> CD154 extracellular domain long form amino acids 108(Glu) to
261(Leu) + Glu binds CD40

<400> 23

Met	Leu	Tyr	Thr	Ser	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Phe	Trp	Ile	Ser	-20	-15	-10	-5
Ala	Ser	Arg	Ser	Met	Leu	Leu	Gly	Ile	Leu	Met	Ile	Cys	Ser	Ala	Thr	-1	1	5	10
Glu	Lys	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Arg	Glu	15	20	25	
Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	Asp	Thr	30	35	40	
Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro	45	50	55	60
Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Asn	Phe	Asn	Met	65	70	75	
Trp	Lys	Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu	80	85	90	
Trp	Asp	Glu	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	95	100	105	
Thr	Leu	Asn	Cys	Thr	Asn	Leu	Asn	Ile	Thr	Lys	Asn	Thr	Thr	Asn	Pro	110	115	120	
Thr	Ser	Ser	Ser	Trp	Gly	Met	Met	Glu	Lys	Gly	Glu	Ile	Lys	Asn	Cys	125	130	135	140
Ser	Phe	Tyr	Ile	Thr	Thr	Ser	Ile	Arg	Asn	Lys	Val	Lys	Lys	Glu	Tyr	145	150	155	
Ala	Leu	Phe	Asn	Arg	Leu	Asp	Val	Val	Pro	Ile	Glu	Asn	Thr	Asn	Asn	160	165	170	

Thr Lys Tyr Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala
 175 180 185
 Cys Pro Lys Val Ser Phe Gln Pro Ile Pro Ile His Tyr Cys Val Pro
 190 195 200
 Ala Gly Phe Ala Met Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Ser
 205 210 215 220
 Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
 225 230 235
 Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu
 240 245 250
 Asp Ile Val Ile Arg Ser Glu Asn Phe Thr Asp Asn Ala Lys Thr Ile
 255 260 265
 Ile Val Gln Leu Asn Glu Ser Val Val Ile Asn Cys Thr Arg Pro Asn
 270 275 280
 Asn Asn Thr Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr
 285 290 295 300
 Ala Arg Arg Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile
 305 310 315
 Ser Arg Ala Lys Trp Asn Asn Thr Leu Gln Gln Ile Val Ile Lys Leu
 320 325 330
 Arg Glu Lys Phe Arg Asn Lys Thr Ile Ala Phe Asn Gln Ser Ser Gly
 335 340 345
 Gly Asp Pro Glu Ile Val Met His Ser Phe Asn Cys Gly Gly Glu Phe
 350 355 360
 Phe Tyr Cys Asn Thr Ala Gln Leu Phe Asn Ser Thr Trp Asn Val Thr
 365 370 375 380
 Gly Gly Thr Asn Gly Thr Glu Gly Asn Asp Ile Ile Thr Leu Gln Cys
 385 390 395
 Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Lys Ala Met
 400 405 410
 Tyr Ala Pro Pro Ile Thr Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr
 415 420 425
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn Ser Thr Glu Thr Glu Thr
 430 435 440
 Glu Ile Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser
 445 450 455 460
 Glu Leu Tyr Lys Tyr Lys Val Val Arg Ile Glu Pro Ile Gly Val Ala
 465 470 475

```

Pro Thr Arg Ala Lys Arg Arg Thr Val Gln Arg Glu Lys Arg Pro Asp
      480                      485                      490

Pro Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile
      495                      500                      505

Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu
      510                      515                      520

Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr
      525                      530                      535                      540

Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr
      545                      550                      555

Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln
      560                      565                      570

Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu
      575                      580                      585

Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys
      590                      595                      600

Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly
      605                      610                      615                      620

Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly
      625                      630                      635

Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
      640                      645

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<210> 24
<211> 294
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      HIV-human fusion construct

<220>
<221> SIGNAL
<222> (1)..(20)
<223> Synthetic secretory signal peptide

<220>
<221> DOMAIN
<222> (21)..(77)
<223> HIV gp120 V3 loop with (Gly4Ser)3 linker

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<220>

<221> BINDING

<222> (80)..(294)

<223> CD154 extracellular domain long form amino acids 48(Arg) to 261(Leu) + Glu binds CD40

<400> 24

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Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20              -15              -10              -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
      -1    1              5              10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
      15              20              25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Gly Gly
      30              35              40

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Arg
      45              50              55              60

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
      65              70              75

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
      80              85              90

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
      95              100             105

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
      110             115             120

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
      125             130             135             140

Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
      145             150             155

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
      160             165             170

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
      175             180             185

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
      190             195             200

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
      205             210             215             220

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
      225             230             235

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
      240             245             250

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Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
 95 100 105
 Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
 110 115 120
 Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
 125 130 135 140
 Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
 145 150 155
 Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
 160 165 170
 Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
 175 180 185
 Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
 190 195 200
 Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
 205 210 215 220
 Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
 225 230 235
 Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr
 240 245 250
 Ser Phe Gly Leu Leu Lys Leu Glu
 255 260

<210> 26

<211> 234

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(77)

<223> HIV gp120 V3 loop with (Gly4Ser)3 linker

<220>

<221> BINDING

<222> (80)..(234)

<223> CD154 extracellular domain long form amino acids 108(Glu) to
261(Leu) + Glu binds CD40

<400> 26

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Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Leu Phe Trp Ile Ser
-20                      -15                      -10                      -5

Ala Ser Arg Ser Val Val Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr
          -1    1                      5                      10

Arg Arg Arg Leu Ser Ile Gly Pro Gly Arg Ala Phe Tyr Ala Arg Arg
      15                      20                      25

Asn Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Ile Ser Gly Gly
      30                      35                      40

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Pro Glu
      45                      50                      55                      60

Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala
          65                      70                      75

His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
          80                      85                      90

Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu
          95                      100                      105

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
      110                      115                      120

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
      125                      130                      135                      140

Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
          145                      150                      155

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
          160                      165                      170

Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
      175                      180                      185

Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
      190                      195                      200

Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
      205                      210

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<210> 27

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
HIV-human fusion construct

<220>

<221> SIGNAL

<222> (1)..(20)

<223> Synthetic secretory signal peptide

<220>

<221> DOMAIN

<222> (21)..(65)

<223> HIV gp120 V3 loop with ProAspPro linker

<220>

<221> BINDING

<222> (66)..(220)

<223> CD154 extracellular domain long form amino acids 108(Glu) to
261(Leu) + Glu binds CD40

<400> 27

Met	Leu	Tyr	Thr	Ser	Gln	Leu	Leu	Gly	Leu	Leu	Phe	Trp	Ile	Ser	-20	-15	-10	-5	
Ala	Ser	Arg	Ser	Val	Val	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	-1	1	5	10
Arg	Arg	Arg	Leu	Ser	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Arg	Arg	15	20	25	
Asn	Ile	Ile	Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Ser	Pro	Asp	30	35	40	
Pro	Glu	Asn	Ser	Phe	Glu	Met	Gln	Lys	Gly	Asp	Gln	Asn	Pro	Gln	Ile	45	50	55	60
Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	Ser	Lys	Thr	Thr	Ser	Val	Leu	65	70	75	
Gln	Trp	Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	Met	Ser	Asn	Asn	Leu	Val	Thr	80	85	90	
Leu	Glu	Asn	Gly	Lys	Gln	Leu	Thr	Val	Lys	Arg	Gln	Gly	Leu	Tyr	Tyr	95	100	105	
Ile	Tyr	Ala	Gln	Val	Thr	Phe	Cys	Ser	Asn	Arg	Glu	Ala	Ser	Ser	Gln	110	115	120	
Ala	Pro	Phe	Ile	Ala	Ser	Leu	Cys	Leu	Lys	Ser	Pro	Gly	Arg	Phe	Glu	125	130	135	140
Arg	Ile	Leu	Leu	Arg	Ala	Ala	Asn	Thr	His	Ser	Ser	Ala	Lys	Pro	Cys	145	150	155	
Gly	Gln	Gln	Ser	Ile	His	Leu	Gly	Gly	Val	Phe	Glu	Leu	Gln	Pro	Gly	160	165	170	

Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly
 175 180 185

Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu Glu
 190 195 200

<210> 28

<211> 6

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 28

Gly Pro Gly Arg Ala Phe
 1 5

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Linker peptide

<400> 29

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15